

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 22, 2003, 10:02:11 ; Search time 756.244 Seconds
(without alignments)
703.246 Million cell updates/sec

Title: US-09-446-089D-3
Perfect score: 69
Sequence: 1 KKLGYVYQDVEIP 13

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09446089/runat_22122003_100055_23005/app_query.fasta_1.1
059

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09446089_CGN_1_1_5415@runat_22122003_100055_23005 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

identical search repeated in GENSEQ, USPATS, USPGPUBS, and EST databases

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Run on: December 22, 2003, 10:02:11 ; Search time 698.071 Seconds
(without alignments)
703.246 Million cell updates/sec

Title: US-09-446-089D-4
Perfect score: 56
Sequence: 1 KIVYRQMVSSAK 12

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09446089/runat_22122003_100055_23005/app_query.fasta_1.1
059

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09446089_@CGN_1_1_5415_@runat_22122003_100055_23005 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Run on: December 22, 2003, 10:02:11 ; Search time 1047.11 Seconds
(without alignments)
703.246 Million cell updates/sec

Title: US-09-446-089D-5
Perfect score: 101
Sequence: 1 KTPQLFFGRPYRRGDQEF 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09446089/runat_22122003_100055_23005/app_query.fasta_1.1
059

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09446089_@CGN_1_1_5415_@runat_22122003_100055_23005 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Run on: December 22, 2003, 10:02:11 ; Search time 1687.01 Seconds
(without alignments)
703.246 Million cell updates/sec

Title: US-09-446-089D-6
Perfect score: 140
Sequence: 1 KIDFELFXPSTTMRVRRAAHLVDDAYIXK 29

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US09446089/runat_22122003_100055_23005/app_query.fasta_1.1
059

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09446089 @CGN_1_1_5415 @runat_22122003_100055_23005 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Run on: December 22, 2003, 10:02:11 ; Search time 7271.57 Seconds
(without alignments)
703.246 Million cell updates/sec

Title: US-09-446-089D-7
Perfect score: 686
Sequence: 1 RQMVS SAKTPQLFFGRPYRR.....ENAEMVRVKVRDCLDGKKLG 125

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-
Q=/cgn2_1/USPTO_spool/US09446089/runat_22122003_100055_23005/app_query.fasta_1.1
059

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09446089_@CGN_1_1_5415_@runat_22122003_100055_23005 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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FILE 'AGRICOLA, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 11:04:23 ON 08 JAN
2004

L1 15 SEA PLU=ON ((POLYPHENOL(3A) OXIDASE) OR (TYROSINASE)) AND
(SCROPHULARIAC? OR AGALINIS OR AGALINUS OR ALECTRA OR AMPHIANTH
US OR ANGELONIA OR ANTIRRHINUM OR ASARINA OR AUREOLARIA)

L2 10 DUP REM L1 (5 DUPLICATES REMOVED)
D TI 1-10
D IBIB AB 6

L3 0 SEA PLU=ON ((POLYPHENOL(3A) OXIDASE) OR (TYROSINASE)) AND
(BACOPA OR BARTSIA OR BELLARDIA OR BESSEYA OR BRACHYSTIGMA OR
BUCHNERA OR CALCEOLARIA OR CAPRARIA OR CASTILLEJA OR CHAENORRHI
NUM OR CHELONE OR CHIONOPHILA OR COLLINSIA OR CORDYLANTHUS OR
CYMBALARIA)

L4 10 SEA PLU=ON ((POLYPHENOL(3A) OXIDASE) OR (TYROSINASE)) AND
(DASISTOMA OR DIASCIA OR DIGITALIS OR DIPLACUS OR DOPATRIUM OR
EPIXIPHUM OR ERINUS OR EUPHRASIA)

L5 9 DUP REM L4 (1 DUPLICATE REMOVED)
D TI 1-9
D IBIB AB 9

L6 1 SEA PLU=ON ((POLYPHENOL(3A) OXIDASE) OR (TYROSINASE)) AND
(FREYLINIA OR GAMBELIA OR GRATIOLA OR HEBE OR HOLMGRENANTHE OR
HOWELLIELLA OR KECKIELLA OR KICKXIA OR LAGOTIS OR LATHRAEA OR
LENDNERIA OR LEUCOPHYLLUM OR LEUCOSPORA OR LIMNOPHILA OR
LIMOSELLA OR LINARIA OR LINDERNIA)
D IBIB AB

L7 0 SEA PLU=ON ((POLYPHENOL(3A) OXIDASE) OR (TYROSINASE)) AND
(MACRANTHERA OR MAURANDELLA OR MAURANDYA OR MAZUS OR MECARDONIA
OR MELAMPYRUM OR MICRANTHEMUM OR MIMETANTHE OR MIMULUS OR
MISOPATES OR MOHAVEA OR NEMESIA OR NEOGAERRHINUM OR NOTHOCHELON
E OR NUTTALLANTHUS)

L8 2 SEA PLU=ON ((POLYPHENOL(3A) OXIDASE) OR (TYROSINASE)) AND
(ODONTITES OR ORTHOCARPUS OR PARENTUCELLIA OR PAULOWNIA OR
PEDICULARIS OR PENSTEMON OR PHYGELIUS OR PSEUDORONTIUM OR
RHEMANNIA OR RHINANTHUS OR RHODOCHITON OR RUSSELIA)
D TI 1-2

L9 1 SEA PLU=ON ((POLYPHENOL(3A) OXIDASE) OR (TYROSINASE)) AND
(SAIROCARPUS OR SCHISTOPHRAGMA OR SCHLEGELIA OR SCHWALBEA OR
SCOPARIA OR SCROPHULARIA OR SELAGO OR SEYMERIA OR SIPHONOSTEGIA
OR STEMODIA OR STRIGA OR SYNTHYRIS OR TONELLA OR TORENIA OR
TRIPHYSARIA OR VERBASCUM OR VERONICA OR VERONICASTRUM)
D IBIB AB